



# 6

## SEQUENCE LISTING

<110> Denney, Jr., Dan W.  
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<140> 09/925,664  
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<150> 09/370,453  
<151> 1999-08-09  
<150> 08/644,664  
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 Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly Leu  
 30 35 40  
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 Phe Phe Ala Asp Leu Leu Asp Tyr Ile Lys Ala Leu Asn Arg Asn Ser  
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Asp Thr Gly Lys Thr Met Gln Thr Leu Leu Ser Leu Val Lys Gln Tyr	
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Ser Pro Lys Met Val Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser	
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Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro Asp	
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Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asn	
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35 40 45

Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala  
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Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp  
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Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr  
85 90 95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly  
100 105 110

Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys  
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Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val  
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Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro  
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Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Ser Ser Val Glu  
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Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile  
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cct gag aag aat cga cct tta aag gac aga att aat ata gtt ctc agt 243  
Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser  
65 70 75

aga gaa ctc aaa gaa cca cca cga gga gct cat ttt ctt gcc aaa agt 291  
Arg Glu Leu Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser  
80 85 90

ttg gat gat gcc tta aga ctt att gaa caa ccg gaa ttg gca agt aaa 339  
Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys  
95 100 105

gta gac atg gtt tgg ata gtc gga ggc agt tct gtt tac cag gaa gcc 387  
Val Asp Met Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala  
110 115 120 125

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Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln  
130 135 140

gaa ttt gaa agt gac acg ttt ttc cca gaa att gat ttg ggg aaa tat 483  
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Lys Leu Leu Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu  
160 165 170

aaa ggc atc aag tat aag ttt gaa gtc tac gag aag aaa gac 573  
Lys Gly Ile Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp  
175 180 185

taacaggaag atgctttcaa gttctctgct cccctcctaa agctatgcat ttttataaga 633  
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Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln  
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Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys  
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Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu  
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Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp  
85 90 95

Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met  
100 105 110

Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln  
115 120 125

Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu  
130 135 140

Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu  
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Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys  
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Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu  
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Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu  
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Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro  
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Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn  
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Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val  
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Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr  
 145 150 155 160

130  
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Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu  
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Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His  
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Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro  
195 200 205

Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg  
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Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr	
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Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn	
35 40 45	
ggg acg gag cgg gtg cgg ttg ctg gaa aga tgc atc tat aac caa gag	192
Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu	
50 55 60	
gag tcc gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtt gag	240
Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu	
65 70 75 80	
gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc	288
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu	
85 90 95	
ctg gag cag aag cgg ggc cag gtg gac aat tac tgc aga cac aac tac	336
Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr	
100 105 110	
ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtt gag cct aag gtg	384
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val	
115 120 125	
act gtg tat cct tca aag acc cag ccc ctg cag cac cac aac ctc ctg	432
Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu	
130 135 140	
gtc tgc tct gtg agt ggt ttc tat cca ggc agc att gaa gtc agg tgg	480
Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp	
145 150 155 160	
ttc cgg aac ggc cag gaa gag aag gct ggg gtg gtg tcc acg ggc ctg	528
Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu	
165 170 175	
atc cag aat gga gat tgg acc ttc cag acc ctg gtg atg ctg gaa ata	576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile	
180 185 190	
gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agt	624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	
195 200 205	
gtg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca	672
Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	
210 215 220	

cca aat aaa gga agt gga acc act tca ggt act acc cgt ctt cta tct	720
Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser	
225 230 235 240	

ggg cac acg tgt ttc acg ttg aca ggt ttg ctt ggg acg cta gta acc	768
Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr	
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Met Gly Leu Leu Thr	
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<211> 261

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<213> Artificial Sequence

<220>

<223> Synthetic

<400> 30

Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr
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Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr
20 25 30

Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn
35 40 45

Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu
50 55 60

Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu
65 70 75 80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
85 90 95

Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr
100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val
115 120 125

Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
130 135 140

Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp  
145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu  
165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile  
180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser  
195 200 205

Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala  
210 215 220

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser  
225 230 235 240

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr  
245 250 255

Met Gly Leu Leu Thr  
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Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu  
1 5 10 15

48

cca ttt tgg gaa gat act aca gag aac gtg gtg tgt gcc ctg ggc ctg  
Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu  
20 25 30

96

act gtg ggt ctg gtg ggc atc att att ggg acc atc ttc atc atc aag 144  
 Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys  
           35                          40                          45

gga gtg cgc aaa agc aat gca gca gaa cgc agg ggg cct ctg taa 189  
 Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu  
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<210> 32

<211> 62

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 32

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu  
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Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu  
                           20                          25                          30

Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys  
           35                          40                          45

Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu  
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<210> 33

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 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu  
 1 5 10 15

cca ttt tgg gaa gat cag agc aag atg ctg agt gga gtc ggg ggc ttc 96  
 Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe  
 20 25 30

gtg ctg ggc ctg ctc ttc ctt ggg gcc ggg ctg ttc atc tac ttc agg 144  
 Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg  
 35 40 45

aat cag aaa gga cac tct gga ctt cag cca aca gga ttc ctg agc tga 192  
 Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser  
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<210> 34

<211> 63

<212> PRT

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<400> 34

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu  
 1 5 10 15

Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe  
 20 25 30

Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg  
 35 40 45

Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser  
 50 55 60

<210> 35

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 35

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39

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 gagaaacctg tgtgttcctt tgggtcaacac cgagacattt aggtgaaaga catctaattc 180  
 tgggttttacg aatctggaaa cttcttgaaa atgtaattct tgagttaaca cttctgggtg 240  
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 <400> 42  
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<400> 43  
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 agcggcggca ccgccgccct gggctgacct gtgaaggact acttccccga gcccgtagacc 120  
 gtgagctgga acagcggcgc cctgaccagc ggcgtccaca cttccccgc cgtgctgcag 180  
 tccagcggcc tgtactccct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 240  
 cagacctaca cctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagcgcgtg 300  
 gagctgaaga cccccctggg cgacaccacc cacacctgcc cccgctgccc cgagcccaag 360  
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 cccccctgcc cccgctgccc cgagcccaag agctgcgaca cccctcccc ctgccccgc 480  
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 accaagcccc gcgaggagca gtacaacagc accttccgcg tggtagagct gctgaccgtg 720  
 ctgcaccagg actggctgaa cggcaaggag tacaagtga aggtgagcaa caaggccctg 780  
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 tagatct 1147



<210> 45

<211> 377

<212> PRT

<213> Homo sapiens

<400> 45

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
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Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro  
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg  
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys  
130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro  
145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr  
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His  
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln  
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met  
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn  
305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu  
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile  
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln  
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
370 375

<210> 46

<211> 999

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 46

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ccgtgagctg gaacagcggc gccctgacca gcggcgtgca caccttcccc gccgtgctgc 180

agagcagcgg cctgtactcc ctgagcagcg tggtgaccgt gcccagcagc agcctgggca 240  
 ccaagaccta cacctgcaac gtggaccaca agcccagcaa caccaaggtg gacaagcgcg 300  
 tggagagcaa gtacggcccc cctgccccca gctgccccgc ccccgagttc ctgggcggcc 360  
 ccagcgtggt cctgttcccc cccaagccca aggacaccct gatgatcagc cgcacccccg 420  
 aggtgacctg cgtggtggtg gacgtgagcc aggaggaccc cgaggtgcag ttcaactggt 480  
 acgtggacgg cgtggaggtg cataacgcca agaccaagcc ccgcgaggag cagttcaaca 540  
 gcacctaccg cgtggtgagc gtgctgaccg tgctgcacca ggactggctg aacggcaagg 600  
 agtacaagtg caaggtgtcc aacaagggcc tgcccagcag catcgagaag accatcagca 660  
 aggccaaagg ccagccccgc gagccccagg tgtacaccct gccccccagc caggaggaga 720  
 tgaccaagaa ccaggtgagc ctgacctgcc tggngaaggg cttctacccc agcgacatcg 780  
 ccgtggagtg ggagagcaac ggccagcccg agaacaacta caagaccacc cccccgtgc 840  
 tggacagcga cggcagcttc ttctgtaca gccgcctgac cgtggacaag agccgctggc 900  
 aggagggcaa cgtgttctcc tgctccgtga tgcattgagg cctgcacaac cactacaccc 960  
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<210> 47

<211> 327

<212> PRT

<213> Homo sapiens

<400> 47

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr  
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro  
 100 105 110  
 Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 115 120 125  
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 130 135 140  
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp  
 145 150 155 160  
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe  
 165 170 175  
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
 180 185 190  
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu  
 195 200 205  
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
 210 215 220  
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys  
 225 230 235 240  
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 245 250 255  
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 260 265 270  
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 275 280 285  
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser  
 290 295 300  
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 305 310 315 320  
 Leu Ser Leu Ser Leu Gly Lys  
 325

<210> 48

<211> 337

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 48

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tgcagtggaa ggtggacaac gccctccaga gcggcaactc ccaggagagc gtgaccgagc      180
aggacagcaa ggacagcacc tacagcctga gcagcaccct gaccctgagc aaggccgact      240
acgagaagca caaggtgtac gcctgcgagg tgacctatca gggcctgagc agccccgtga      300
ccaagagctt caaccggggc gagtgctagt gagatct      337
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<210> 49

<211> 106

<212> PRT

<213> Homo sapiens

<400> 49

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Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
          20           25           30
```

```
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
          35           40           45
```

```
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50           55           60
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```
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65           70           75           80
```

```
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85           90           95
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```
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100          105
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134  
-291

<210> 50  
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 ccggggccgt gaccgtggcc tggaaggccg acagcagccc cgtgaaggcc ggcgtggaga 180  
 ccaccacccc cagcaagcag agcaacaaca agtacgccgc cagcagctac ctgagcctga 240  
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<210> 51  
 <211> 109  
 <212> PRT  
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 <400> 51  
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 Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
 35 40 45  
 Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln  
 50 55 60  
 Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu  
 65 70 75 80  
 Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
 85 90 95  
 Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
 100 105

<210> 52  
 <211> 38  
 <212> DNA  
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<210> 56  
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 <400> 59  
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<210> 60  
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<210> 68  
 <211> 43  
 <212> DNA  
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17